

SEQUENCE LISTING

(1) GENERAL INFORMATION

(i) APPLICANT: Hillman, Jennifer L.  
Yue, Henry  
Lal, Preeti  
Shah, Purvi  
Corley, Neil C.

(ii) TITLE OF THE INVENTION: PROTEINS ASSOCIATED WITH CELL PROLIFERATION

(iii) NUMBER OF SEQUENCES: 9

(iv) CORRESPONDENCE ADDRESS:

(A) ADDRESSEE: Incyte Pharmaceuticals, Inc.  
(B) STREET: 3174 Porter Dr.  
(C) CITY: Palo Alto  
(D) STATE: CA  
(E) COUNTRY: USA  
(F) ZIP: 94304

(v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: Diskette  
(B) COMPUTER: IBM Compatible  
(C) OPERATING SYSTEM: DOS  
(D) SOFTWARE: FastSEQ for Windows Version 2.0

(vi) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER: To Be Assigned  
(B) FILING DATE: Filed Herewith

(vii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER:  
(B) FILING DATE:

(viii) ATTORNEY/AGENT INFORMATION:

(A) NAME: Billings, Lucy J.  
(B) REGISTRATION NUMBER: 36,749  
(C) REFERENCE/DOCKET NUMBER: PF-0421 US

(ix) TELECOMMUNICATION INFORMATION:

(A) TELEPHONE: 650-855-0555  
(B) TELEFAX: 650-845-4166

(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 168 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(vii) IMMEDIATE SOURCE:

(A) LIBRARY: SYNORAB01  
(B) CLONE: 358673

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

Met	Phe	Gln	Ile	Pro	Glu	Phe	Glu	Pro	Ser	Glu	Gln	Glu	Asp	Ser	Ser
1				5				10						15	
Ser	Ala	Glu	Arg	Gly	Leu	Gly	Pro	Ser	Pro	Ala	Gly	Asp	Gly	Pro	Ser
			20					25					30		

Gly Ser Gly Lys His His Arg Gln Ala Pro Gly Leu Leu Trp Asp Ala  
           35                          40                          45  
 Ser His Gln Gln Glu Gln Pro Thr Ser Ser Ser His His Gly Gly Ala  
           50                          55                          60  
 Gly Ala Val Glu Ile Arg Ser Arg His Ser Ser Tyr Pro Ala Gly Thr  
   65                          70                          75                          80  
 Glu Asp Asp Glu Gly Met Gly Glu Glu Pro Ser Pro Phe Arg Gly Arg  
           85                          90                          95  
 Ser Arg Ser Ala Pro Pro Asn Leu Trp Ala Ala Gln Arg Tyr Gly Arg  
          100                         105                         110  
 Glu Leu Arg Arg Met Ser Asp Glu Phe Val Asp Ser Phe Lys Lys Gly  
          115                         120                         125  
 Leu Pro Arg Pro Lys Ser Ala Gly Thr Ala Thr Gln Met Arg Gln Ser  
          130                         135                         140  
 Ser Ser Trp Thr Arg Val Phe Gln Ser Trp Trp Asp Arg Asn Leu Gly  
  145                         150                         155                         160  
 Arg Gly Ser Ser Ala Pro Ser Gln  
                          165

## (2) INFORMATION FOR SEQ ID NO:2:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1105 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

## (vii) IMMEDIATE SOURCE:

- (A) LIBRARY: 358673  
 (B) CLONE: SYNORAB01

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

CGACCGTCCG	CGGGAGACTG	AGGTCCTGAG	CCGACAGCCT	CAGCTCCCTG	CCAGGCCAGA	60
CCCGGCAGAC	AGATGAGGGC	CCAGGAGGCC	TGGCGGGCCT	GGGGGCGCTA	CGGTGGGAGA	120
GGAAGCCAGG	GGTACCTGCC	TCTGCCTTCC	AGGGCCACCG	TTGGCCCCAG	CTGTGCCTTG	180
ACTACGTAAC	ATCTTGTCCT	CACAGCCCAG	AGCATGTTCC	AGATCCCAGA	GTTTGAGCCG	240
AGTGAGCAGG	AAGACTCCAG	CTCTGCAGAG	AGGGGCCTGG	GCCCCAGCCC	CGCAGGGGAC	300
GGGCCCTCAG	GCTCCGGCAA	GCATCATCGC	CAGGCCCCAG	GCCTCCTGTG	GGACGCCAGT	360
CACCAGCAGG	AGCAGCCAAC	CAGCAGCAGC	CATCATGGAG	GCGCTGGGGC	TGTGGAGATC	420
CGGAGTCGCC	ACAGCTCCTA	CCCCGCGGGG	ACGGAGGACG	ACGAAGGGAT	GGGGGAGGAG	480
CCCAGCCCCCT	TTCGGGGCCG	CTCGCGCTCG	GCGCCCCCCA	ACCTCTGGGC	AGCACAGCGC	540
TATGGCCGCG	AGCTCCGGAG	GATGAGTGAC	GAGTTTGTGG	ACTCCTTTAA	GAAGGGACTT	600
CCTCGCCCGA	AGAGCGCGGG	CACAGCAACG	CAGATGCGGC	AAAGCTCCAG	CTGGACGCGA	660
GTCTTCCAGT	CCTGGTGGGA	TCGGAAGTTG	GGCAGGGGAA	GCTCCGCCCC	CTCCCAGTGA	720
CCTTCGCTCC	ACATCCCGAA	ACTCCACCCG	TTCCCACTGC	CCTGGGCAGC	CATCTTGAAT	780
ATGGGCGGAA	GTACTTCCCT	CAGGCCTATG	CAAAAAGAGG	ATCCGTGCTG	TCTCCTTTGG	840
AGGGAGGGCT	GACCCAGATT	CCCTTCCGGT	GCGTGTGAAG	CCACGGAAGG	CTTGGTCCCA	900
TCGGAAGTTT	TGGGTTTTC	GCCCACAGCC	GCCGGAAGTG	GCTCCGTGGC	CCCGCCCTCA	960
GGCTCCGGGC	TTTCCCCCAG	GCGCCTGCGC	TAAGTCGCGA	GCCAGGTTTA	ACCGTTGCGT	1020
CACCGGGACC	CGAGCCCCCG	CGATGCCCTG	GGGGCCGTGC	TCACTACCAA	ATGTTAATAA	1080
AGCCCGCGTC	TGTGCAAAAA	AAAAA				1105

## (2) INFORMATION FOR SEQ ID NO:3:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 440 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

## (vii) IMMEDIATE SOURCE:

- (A) LIBRARY: LATRTUT02  
 (B) CLONE: 1352286

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

Met Arg Val Val Thr Ile Val Ile Leu Leu Cys Phe Cys Lys Ala Ala  
 1 5 10 15  
 Glu Leu Arg Lys Ala Ser Pro Gly Ser Val Arg Ser Arg Val Asn His  
 20 25 30  
 Gly Arg Ala Gly Gly Gly Arg Arg Gly Ser Asn Pro Val Lys Arg Tyr  
 35 40 45  
 Ala Pro Gly Leu Pro Cys Asp Val Tyr Thr Tyr Leu His Glu Lys Tyr  
 50 55 60  
 Leu Asp Cys Gln Glu Arg Lys Leu Val Tyr Val Leu Pro Gly Trp Pro  
 65 70 75 80  
 Gln Asp Leu Leu His Met Leu Leu Ala Arg Asn Lys Ile Arg Thr Leu  
 85 90 95  
 Lys Asn Asn Met Phe Ser Lys Phe Lys Lys Leu Lys Ser Leu Asp Leu  
 100 105 110  
 Gln Gln Asn Glu Ile Ser Lys Ile Glu Ser Glu Ala Phe Phe Gly Leu  
 115 120 125  
 Asn Lys Leu Thr Thr Leu Leu Gln His Asn Gln Ile Lys Val Leu  
 130 135 140  
 Thr Glu Glu Val Phe Ile Tyr Thr Pro Leu Leu Ser Tyr Leu Arg Leu  
 145 150 155 160  
 Tyr Asp Asn Pro Trp His Cys Thr Cys Glu Ile Glu Thr Leu Ile Ser  
 165 170 175  
 Met Leu Gln Ile Pro Arg Asn Arg Asn Leu Gly Asn Tyr Ala Lys Cys  
 180 185 190  
 Glu Ser Pro Gln Glu Gln Lys Asn Lys Lys Leu Arg Gln Ile Lys Ser  
 195 200 205  
 Glu Gln Leu Cys Asn Glu Glu Lys Glu Gln Leu Asp Pro Lys Pro Gln  
 210 215 220  
 Val Ser Gly Arg Pro Pro Val Ile Lys Pro Glu Val Asp Ser Thr Phe  
 225 230 235 240  
 Cys His Asn Tyr Val Phe Pro Ile Gln Thr Leu Asp Cys Lys Arg Lys  
 245 250 255  
 Glu Leu Lys Lys Val Pro Asn Asn Ile Pro Pro Asp Ile Val Lys Leu  
 260 265 270  
 Asp Leu Ser Tyr Asn Lys Ile Asn Gln Leu Arg Pro Lys Glu Phe Glu  
 275 280 285  
 Asp Val His Glu Leu Lys Lys Leu Asn Leu Ser Ser Asn Gly Ile Glu  
 290 295 300  
 Phe Ile Asp Pro Ala Ala Phe Leu Gly Leu Thr His Leu Glu Glu Leu  
 305 310 315 320  
 Asp Leu Ser Asn Asn Ser Leu Gln Asn Phe Asp Tyr Gly Val Leu Glu  
 325 330 335  
 Asp Leu Tyr Phe Leu Lys Leu Leu Trp Leu Arg Asp Asn Pro Trp Arg  
 340 345 350  
 Cys Asp Tyr Asn Ile His Tyr Leu Tyr Tyr Trp Leu Lys His His Tyr  
 355 360 365  
 Asn Val His Phe Asn Gly Leu Glu Cys Lys Thr Pro Glu Glu Tyr Lys  
 370 375 380  
 Gly Trp Ser Val Gly Lys Tyr Ile Arg Ser Tyr Tyr Glu Glu Cys Pro  
 385 390 395 400  
 Lys Asp Lys Leu Pro Ala Tyr Pro Glu Ser Phe Asp Gln Asp Thr Glu  
 405 410 415  
 Asp Asp Glu Trp Glu Lys Lys His Arg Asp His Thr Ala Lys Lys Gln  
 420 425 430  
 Ser Val Ile Ile Thr Ile Val Gly  
 435 440

## (2) INFORMATION FOR SEQ ID NO:4:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2082 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (vii) IMMEDIATE SOURCE:

(A) LIBRARY: LATRTUT02

(B) CLONE: 1352286

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

GAATGCAGCC CATTCTCTGG AGAACTTCCT CACACACCGC AGCAAAGAGA AGACTGAAAG 60  
 ACAAACCTGG GTGCAGCCAG AGAGGTCCAG ATAGATGAGC TTGTGGCATC CATTCCCCAA 120  
 GTTCAGCCTA GGGACTCCAC GTACCCACAG TGGGTCTCAT TGTTCAGAA CTGCATTAGT 180  
 TAAGATTACC CAGACTTGGA TTTCAAAGGA ATACTTTTCAT TGTTCCTCT GTAACACGAA 240  
 GTAATTGGGG CCAGCTGGAT GTCAGGATGC GTGTGGTTAC CATTGTAATC TTGCTCTGCT 300  
 TTTGCAAAGC GGCTGAGCTG CGCAAAGCAA GCCCAGGCAG TGTGAGAAGC CGAGTGAATC 360  
 ATGGCCGGGC GGGTGGAGGC CGGAGAGGCT CCAACCCGGT CAAACGCTAC GCACCAGGCC 420  
 TCCCGTGTGA CGTGACACA TATCTCCATG AGAAATACCT AGATTGTCAA GAAAGAAAAT 480  
 TAGTTTATGT GCTGCTGGT TGGCCTCAGG ATTTGCTGCA CATGCTGCTA GCAAGAAACA 540  
 AGATCCGCAC ATTGAAGAAC AACATGTTTT CCAAGTTTAA AAAGCTGAAA AGCCTGGATC 600  
 TGCAGCAGAA TGAGATCTCT AAAATTGAGA GTGAGGCGTT CTTTGGTTTA AACAAACTCA 660  
 CCACCTCTTT ACTGCAGCAC AACCAGATCA AAGTCTTGAC GGAGGAAGTG TTCATTTACA 720  
 CACCTCTCTT GAGCTACCTG CGTCTTTATG ACAACCCCTG GCACTGTACT TGTGAGATAG 780  
 AAACGCTTAT TTCAATGTTG CAGATTCCCA GGAACCGGAA TTTGGGGAAC TACGCCAAGT 840  
 GTGAAAGTCC ACAAGAACAA AAAAATAAAA AACTGCGGCA GATAAAATCT GAACAGTTGT 900  
 GTAATGAAGA AAAGGAACAA TTGGACCCGA AACCCCAAGT GTCAGGGAGA CCCCCAGTCA 960  
 TCAAGCCTGA GGTGGACTCA ACTTTTGGCC ACAATTATGT GTTTCCTATA CAAACACTGG 1020  
 ACTGCAAAAG GAAAGAGTTG AAAAAGTGC CAAACAACAT CCCTCCAGAT ATTGTTAAAC 1080  
 TTGACTTGTC ATACAATAAA ATCAACCAAC TTCGACCCAA GGAATTTGAA GATGTTTCATG 1140  
 AGCTGAAGAA ATTAAACCTC AGCAGCAATG GCATTGAATT CATCGATCCT GCCGCTTTTT 1200  
 TAGGGCTCAC ACATTTAGAA GAATTAGATT TATCAAACAA CAGTCTGCAA AACTTTGACT 1260  
 ATGGCGTATT AGAAGACTTG TATTTTTTGA AACTCTTGTC GCTCAGAGAT AACCTTGGA 1320  
 GATGTGACTA CAACATTCAC TACCTCTACT ACTGGTTAAA GCACCACTAC AATGTCCATT 1380  
 TTAATGGCCT GGAATGCAAA ACGCCTGAAG AATACAAAGG ATGGTCTGTG GGAAAATATA 1440  
 TTAGAAGTTA CTATGAAGAA TGCCCCAAAG ACAAGTTACC AGCATATCCT GAGTCATTTG 1500  
 ACCAAGACAC AGAAGATGAT GAATGGGAAA AAAAACATAG AGATCACACC GCAAAGAAGC 1560  
 AAAGCGTAAT AATTACTATA GTAGGATAAG GTAGAAATTG TTCTGATTGT AATTAGTTTT 1620  
 GTATTTTCTA TACTGGTGT AGAAAACATA TGTTTACATT TGATTAACCTG TGTTGCCTAT 1680  
 TTATGCAGG TAATCCAGCT AAAGGAAGCT TTCTTTAATT ATAAGTATTA TTGTGACTAT 1740  
 TATAGTAATC AAGAGAATGC TATCATCTG CTTGCCTGTC CATTTGTGGA ACAGCATCTG 1800  
 GTGATATGCA ATTCCACACT GGTAACCTGC AGCAGTTGGG TCCTAATGAT GGCATTAGAC 1860  
 TTTTATAATG TCCTGTATA ATGTTTTTAC TGCTTTTAGA AAATAAAGAA AAAAACTTG 1920  
 GTTCATGTTT ACATGCCTTT CGATAGCTGT TTGTGCATAC TTAAAGATGA TCAAAATGAT 1980  
 TTTATACAAA TGCTGTTATA ATAAAATGTC ATTCCCTACC CCTCTACTTT TTTTCAGTAA 2040  
 GTCATCTTAT ACATTAAATA AATTTCCATT TCTGAAAAA AA 2082

## (2) INFORMATION FOR SEQ ID NO:5:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 469 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

## (vii) IMMEDIATE SOURCE:

- (A) LIBRARY: OVARTUT01  
 (B) CLONE: 815087

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

Met Asp Val Glu Asn Glu Gln Ile Leu Asn Val Asn Pro Ala Asp Pro  
 1 5 10 15  
 Asp Asn Leu Ser Asp Ser Leu Phe Ser Gly Asp Glu Glu Asn Ala Gly  
 20 25 30  
 Thr Glu Glu Val Lys Asn Glu Ile Asn Gly Asn Trp Ile Ser Ala Ser  
 35 40 45  
 Ser Ile Asn Glu Ala Arg Ile Asn Ala Lys Ala Lys Arg Arg Leu Arg  
 50 55 60  
 Lys Asn Ser Ser Arg Asp Ser Gly Arg Gly Asp Ser Val Ser Asp Ser  
 65 70 75 80  
 Gly Ser Asp Ala Leu Arg Ser Gly Leu Thr Val Pro Thr Ser Pro Lys

85 90 95  
 Gly Arg Leu Leu Asp Arg Arg Ser Arg Ser Gly Lys Gly Arg Gly Leu  
 100 105 110  
 Pro Lys Lys Gly Gly Ala Gly Gly Lys Gly Val Trp Gly Thr Pro Gly  
 115 120 125  
 Gln Val Tyr Asp Val Glu Glu Val Asp Val Lys Asp Pro Asn Tyr Asp  
 130 135 140  
 Asp Asp Gln Glu Asn Cys Val Tyr Glu Thr Val Val Leu Pro Leu Asp  
 145 150 155 160  
 Glu Arg Ala Phe Glu Lys Thr Leu Thr Pro Ile Ile Gln Glu Tyr Phe  
 165 170 175  
 Glu His Gly Asp Thr Asn Glu Val Ala Glu Met Leu Arg Asp Leu Asn  
 180 185 190  
 Leu Gly Glu Met Lys Ser Gly Val Pro Val Leu Ala Val Ser Leu Ala  
 195 200 205  
 Leu Glu Gly Lys Ala Ser His Arg Glu Met Thr Ser Lys Leu Leu Ser  
 210 215 220  
 Asp Leu Cys Gly Thr Val Met Ser Thr Thr Asp Val Glu Lys Ser Phe  
 225 230 235 240  
 Asp Lys Leu Leu Lys Asp Leu Pro Glu Leu Ala Leu Asp Thr Pro Arg  
 245 250 255  
 Ala Pro Gln Leu Val Gly Gln Phe Ile Ala Arg Ala Val Gly Asp Gly  
 260 265 270  
 Ile Leu Cys Asn Thr Tyr Ile Asp Ser Tyr Lys Gly Thr Val Asp Cys  
 275 280 285  
 Val Gln Ala Arg Ala Ala Leu Asp Lys Ala Thr Val Leu Leu Ser Met  
 290 295 300  
 Ser Lys Gly Gly Lys Arg Lys Asp Ser Val Trp Gly Ser Gly Gly Gly  
 305 310 315 320  
 Gln Gln Ser Val Asn His Leu Val Lys Glu Ile Asp Met Leu Leu Lys  
 325 330 335  
 Glu Tyr Leu Leu Ser Gly Asp Ile Ser Glu Ala Glu His Cys Leu Lys  
 340 345 350  
 Glu Leu Glu Val Pro His Phe His His Glu Leu Val Tyr Glu Ala Ile  
 355 360 365  
 Ile Met Val Leu Glu Ser Thr Gly Glu Ser Thr Phe Lys Met Ile Leu  
 370 375 380  
 Asp Leu Leu Lys Ser Leu Trp Lys Ser Ser Thr Ile Thr Val Asp Gln  
 385 390 395 400  
 Met Lys Arg Gly Tyr Glu Arg Ile Tyr Asn Glu Ile Pro Asp Ile Asn  
 405 410 415  
 Leu Asp Val Pro His Ser Tyr Ser Val Leu Glu Arg Phe Val Glu Glu  
 420 425 430  
 Cys Phe Gln Ala Gly Ile Ile Ser Lys Gln Leu Arg Asp Leu Cys Pro  
 435 440 445  
 Ser Arg Gly Arg Lys Arg Phe Val Ser Glu Gly Asp Gly Gly Arg Leu  
 450 455 460  
 Lys Pro Glu Ser Tyr  
 465

## (2) INFORMATION FOR SEQ ID NO:6:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2395 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (vii) IMMEDIATE SOURCE:

- (A) LIBRARY: OVARTUT01
- (B) CLONE: 815087

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

ACAGCTCGAG CTCGAGCCGC AAAACTGTCT GCAGACGTCA ATTTGCCCC CCTCCCCCTT 60  
 GTGAGAACTC GCTACGTAGC CAGCAACTGT GTAGTGTCTA CAAATGATGA AAACGATCAG 120

AAATGCGATT AGGTGTCGGG GAAAAAAGGG TTTCCCCTGT TTTTAACTTG TATTTTTACT 180  
 TTAATTGTGA CAATCTTGAT ATTCTTAACG TGACTTTTTT GGGAAACCAC CAAGTGCTTT 240  
 TTAAGCAAGG AGTTACTGAT TCTGAAGGAA GATTTCCATT AGGTAATTTG TTTAATCAGT 300  
 GCAAGCGAAA TTAAGGGAAA ATGGATGTAG AAAATGAGCA GATACTGAAT GTAAACCCTG 360  
 CAGATCCTGA TAACTTAAGT GACTCTCTCT TTTCCGGTGA TGAAGAAAAT GCTGGGACTG 420  
 AGGAAGTAAA GAATGAAATA AATGGAAATT GGATTTTCAGC ATCCTCCATT AACGAAGCTA 480  
 GAATTAATGC CAAGGCAAAA AGGCGACTAA GGAAAACTC ATCCCGGGAC TCTGGCAGAG 540  
 GCGATTCGGT CAGCGACAGT GGGAGTGACG CCCTTAGAAG TGGATTAAC GTGCCAACCA 600  
 GTCCAAAGGG AAGGTTGCTG GATAGGCGAT CCAGATCTGG GAAAGGAAGG GGACTACCAA 660  
 AGAAAGGTGG TGCAGGAGGC AAAGGTGTCT GGGGTACACC TGGACAGGTG TATGATGTGG 720  
 AGGAGGTGGA TGTGAAAGAT CCTAACTATG ATGATGACCA GGAGAACTGT GTTTATGAAA 780  
 CTGTAGTTTT GCCTTTGGAT GAAAGGGCAT TTGAGAAGAC TTTAACACCA ATCATACAGG 840  
 AATATTTTGA GCATGGAGAT ACTAATGAAG TTGCGGAAAT GTTAAGAGAT TTAAATCTTG 900  
 GTGAAATGAA AAGTGGAGTA CCAGTGTGG CAGTATCCTT AGCATTGAG GGGAAGGCTA 960  
 GTCATAGAGA GATGACATCT AAGCTTCTTT CTGACCTTTG TGGGACAGTA ATGAGCACAA 1020  
 CTGATGTGGA AAAATCATTT GATAAATTGT TGAAAGATCT ACCTGAATTA GCACTGGATA 1080  
 CTCCTAGAGC ACCACAGTTG GTGGGCCAGT TTATTGCTAG AGCTGTTGGA GATGGAATTT 1140  
 TATGTAATAC CTATATTGAT AGTTACAAAG GAACGTGAGA TTGTGTGCAG GCTAGAGCTG 1200  
 CTCTGGATAA GGCTACCGTG CTTCTGAGTA TGTCTAAAGG TGGAAAGCGT AAAGATAGTG 1260  
 TGTGGGGCTC TGGAGGTGGG CAGCAATCTG TCAATCACCT TGTAAAGAG ATTGATATGC 1320  
 TGCTGAAAGA ATATTTACTC TCTGGAGACA TATCTGAAGC TGAACATTGC CTTAAGGAAC 1380  
 TGGAAGTACC TCATTTTCAC CATGAGCTTG TATATGAAGC TATTATAATG GTTTTAGAGT 1440  
 CAACTGGAGA AAGTACATTT AAGATGATTT TGGATTTATT AAAGTCCCTT TGGAAAGTCTT 1500  
 CTACCATTAC TGTAGACCAA ATGAAAAGAG GTTATGAGAG AATTTACAAT GAAATTCCGG 1560  
 ACATTAATCT GGATGTCCCA CATTCATACT CTGTGCTGGA GCGGTTTGTA GAAGAATGTT 1620  
 TTCAGGCTGG AATAATTTCC AAACAACCTCA GAGATCTTTG TCCTTCAAGG GGCAGAAAGC 1680  
 GTTTTGTAAG CGAAGGAGAT GGAGGTCGTC TTAAACCAGA GAGCTACTGA ATATAAGAAC 1740  
 TCTTGCAGTC TTAGATGTTA TAAAAATATA TATCTGAATT GTAAGAGTTG TTAGCACAAAG 1800  
 TTTTTTTTTT TTTTTTTTTT TAAGCACTTG TTTTGGGTAC AAGGCATTTC TGACATTTTA 1860  
 TAAACCTACA TTTAAGGGGA ATTTTAAAG GAAATGTTTT TTCTTTTTTT TTTGTTTTTC 1920  
 GAGGGGGCAA GGAGGGACAG AAAAGTAACC TCTTCTTAAG TGGAATATTC TAATAAGCTA 1980  
 CCTTTTGTA GTGCCATGTT TATATCTAA TCATTCCAAG TTTTGCATTG ATGTCTGACT 2040  
 GCCACTCCTT TCTTTCAAG ACAGTGTFTT TTGTAGTAAA ATCACTGGTT TATACAAAGC 2100  
 TTTATTTAGG GGGTAAAGTT AAGCTGCTAA AACCCCATGT TGGCTGCTGC TGTGAGATA 2160  
 CTGTGCTTTG GGAGTAAAAA AAGAAAGTTA TTTCTTTGTC TTAAAGAATT TTTAAAAAAT 2220  
 TAGTCATGAG ACTTATTCAT CTTTCCAGGG AACATACTGA TTGGTCTTAA AAGACTAGAC 2280  
 AGTTAAGTAA AAGGTGGCTG GAACATCTAT TTTTCTACAA AACTGGAAAA ATGAACCTGG 2340  
 TTCTAGAAGA ATGTACACCA AAATAAAACA TGTGAAGCAG TATTGAAAAA AAAAA 2395

## (2) INFORMATION FOR SEQ ID NO:7:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 168 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

## (vii) IMMEDIATE SOURCE:

- (A) LIBRARY: GenBank  
 (B) CLONE: 1683637

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

Met Phe Gln Ile Pro Glu Phe Glu Pro Ser Glu Gln Glu Asp Ser Ser  
 1 5 10 15  
 Ser Ala Glu Arg Gly Leu Gly Pro Ser Pro Ala Gly Asp Gly Pro Ser  
 20 25 30  
 Gly Ser Gly Lys His His Arg Gln Ala Pro Gly Leu Leu Trp Asp Ala  
 35 40 45  
 Ser His Gln Gln Glu Gln Pro Thr Ser Ser Ser His His Gly Gly Arg  
 50 55 60  
 Trp Gly Cys Gly Asp Pro Glu Ser Pro Gln Leu Leu Pro Arg Gly Asp  
 65 70 75 80  
 Gly Gly Arg Arg Arg Asp Gly Gly Gly Ala Gln Pro Phe Arg Gly Arg  
 85 90 95  
 Ser Arg Ser Ala Pro Pro Asn Leu Trp Ala Ala Gln Arg Tyr Gly Arg

[illegible]

(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 313 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(vii) IMMEDIATE SOURCE:

- (A) LIBRARY: GenBank  
(B) CLONE: 1236329

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

Met 1	Arg	Val	Val	Thr 5	Ile	Val	Ile	Leu	Leu 10	Cys	Phe	Cys	Lys	Ala 15	Ala
Glu	Leu	Arg	Lys 20	Ala	Ser	Pro	Gly	Ser 25	Val	Arg	Ser	Arg	Val 30	Asn	His
Gly	Arg	Ala 35	Gly	Gly	Gly	Arg	Arg 40	Gly	Ser	Asn	Pro	Val 45	Lys	Arg	Tyr
Ala 50	Pro	Gly	Leu	Pro	Cys	Asp 55	Val	Tyr	Thr	Tyr	Leu 60	His	Glu	Lys	Tyr
Leu 65	Asp	Cys	Gln	Glu	Arg 70	Lys	Leu	Val	Tyr	Val 75	Leu	Pro	Gly	Trp	Pro 80
Gln	Asp	Leu	Leu 85	His	Met	Leu	Leu	Ala 90	Arg	Asn	Lys	Ile	Arg	Thr 95	Leu
Lys	Asn	Asn	Met 100	Phe	Ser	Lys	Phe	Lys 105	Lys	Leu	Lys	Ser	Leu 110	Asp	Leu
Gln	Gln	Asn 115	Glu	Ile	Ser	Lys	Ile 120	Glu	Ser	Glu	Ala	Phe 125	Phe	Gly	Leu
Asn 130	Lys	Leu	Thr	Thr	Leu	Leu 135	Leu	Gln	His	Asn	Gln 140	Ile	Lys	Val	Leu
Thr 145	Glu	Glu	Val	Phe	Ile 150	Tyr	Thr	Pro	Leu	Leu 155	Ser	Tyr	Leu	Arg	Leu 160
Tyr	Asp	Asn	Pro 165	Trp	His	Cys	Thr	Cys 170	Glu	Ile	Glu	Thr	Leu 175	Ile	Ser
Met	Leu	Gln	Ile 180	Pro	Arg	Asn	Arg	Asn 185	Leu	Ala	Asn	Tyr	Ala 190	Lys	Cys
Glu	Ser	Pro 195	Gln	Glu	Gln	Lys	Asn 200	Lys	Lys	Leu	Arg	Gln 205	Ile	Lys	Ser
Glu 210	Gln	Leu	Cys	Asn	Glu	Glu 215	Glu	Lys	Glu	Gln	Leu 220	Asp	Pro	Lys	Pro
Gln 225	Val	Ser	Gly	Arg	Pro 230	Pro	Val	Ile	Lys	Pro 235	Glu	Val	Asp	Ser	Thr 240
Phe	Cys	His	Asn 245	Tyr	Val	Phe	Pro	Ile 250	Gln	Thr	Leu	Asp	Cys 255	Lys	Arg
Lys	Glu	Leu	Lys 260	Lys	Val	Pro	Asn 265	Asn	Ile	Pro	Pro	Asp	Ile 270	Val	Lys
Leu	Asp	Leu 275	Ser	Tyr	Asn	Lys	Ile 280	Asn	Gln	Leu	Arg	Pro 285	Lys	Glu	Phe
Glu 290	Asp	Val	His	Glu	Leu	Lys 295	Lys	Leu	Asn	Leu	Ser 300	Ser	Asn	Gly	Ile
Glu 305	Phe	Ile	Asp	Pro	Gly 310	Ser	Leu	Arg							

## (2) INFORMATION FOR SEQ ID NO:9:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 469 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

## (vii) IMMEDIATE SOURCE:

- (A) LIBRARY: GenBank  
 (B) CLONE: 1384078

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

```

Met Asp Ile Glu Asn Glu Gln Thr Leu Asn Val Asn Pro Thr Asp Pro
 1      5      10      15
Asp Asn Leu Ser Asp Ser Leu Phe Ser Gly Asp Glu Glu Asn Ala Gly
 20      25      30
Thr Glu Glu Ile Lys Asn Glu Ile Asn Gly Asn Trp Ile Ser Ala Ser
 35      40      45
Thr Ile Asn Glu Ala Arg Ile Asn Ala Lys Ala Lys Arg Arg Leu Arg
 50      55      60
Lys Asn Ser Ser Arg Asp Ser Gly Arg Gly Asp Ser Val Ser Asp Asn
 65      70      75      80
Gly Ser Glu Ala Val Arg Ser Gly Val Ala Val Pro Thr Ser Pro Lys
 85      90      95
Gly Arg Leu Leu Asp Arg Arg Ser Arg Ser Gly Lys Gly Arg Gly Leu
 100     105     110
Pro Lys Lys Gly Gly Ala Gly Gly Lys Gly Val Trp Gly Thr Pro Gly
 115     120     125
Gln Val Tyr Asp Val Glu Glu Val Asp Val Lys Asp Pro Asn Tyr Asp
 130     135     140
Asp Asp Gln Glu Asn Cys Val Tyr Glu Thr Val Val Leu Pro Leu Asp
 145     150     155     160
Glu Thr Ala Phe Glu Lys Thr Leu Thr Pro Ile Ile Gln Glu Tyr Phe
 165     170     175
Glu His Gly Asp Thr Asn Glu Val Ala Glu Met Leu Arg Asp Leu Asn
 180     185     190
Leu Gly Glu Met Lys Ser Gly Val Pro Val Leu Ala Val Ser Leu Ala
 195     200     205
Leu Glu Gly Lys Ala Ser His Arg Glu Met Thr Ser Lys Leu Leu Ser
 210     215     220
Asp Leu Cys Gly Thr Val Met Ser Thr Asn Asp Val Glu Lys Ser Phe
 225     230     235     240
Asp Lys Leu Leu Lys Asp Leu Pro Glu Leu Ala Leu Asp Thr Pro Arg
 245     250     255
Ala Pro Gln Leu Val Gly Gln Phe Ile Ala Arg Ala Val Gly Asp Gly
 260     265     270
Ile Leu Cys Asn Thr Tyr Ile Asp Ser Tyr Lys Gly Thr Val Asp Cys
 275     280     285
Val Gln Ala Arg Ala Ala Leu Asp Lys Ala Thr Val Leu Leu Ser Met
 290     295     300
Ser Lys Gly Gly Lys Arg Lys Asp Ser Val Trp Gly Ser Gly Gly Gly
 305     310     315     320
Gln Gln Pro Val Asn His Leu Val Lys Glu Ile Asp Met Leu Leu Lys
 325     330     335
Glu Tyr Leu Leu Ser Gly Asp Ile Ser Glu Ala Glu His Cys Leu Lys
 340     345     350
Glu Leu Glu Val Pro His Phe His His Glu Leu Val Tyr Glu Ala Ile
 355     360     365
Val Met Val Leu Glu Ser Thr Gly Glu Ser Ala Phe Lys Met Ile Leu
 370     375     380
Asp Leu Leu Lys Ser Leu Trp Lys Ser Ser Thr Ile Thr Ile Asp Gln
 385     390     395     400
Met Lys Arg Gly Tyr Glu Arg Ile Tyr Asn Glu Ile Pro Asp Ile Asn
 405     410     415

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Leu	Asp	Val	Pro	His	Ser	Tyr	Ser	Val	Leu	Glu	Arg	Phe	Val	Glu	Glu
			420					425					430		
Cys	Phe	Gln	Ala	Gly	Ile	Ile	Ser	Lys	Gln	Leu	Arg	Asp	Leu	Cys	Pro
		435					440					445			
Ser	Arg	Gly	Arg	Lys	Arg	Phe	Val	Ser	Glu	Gly	Asp	Gly	Gly	Arg	Leu
		450				455					460				
Lys	Pro	Glu	Ser	Tyr											
465															

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